

CLAIMS

1. A variant of a parent α -amylase, which parent α -amylase (i) has an amino acid sequence selected from the amino acid sequences shown in SEQ ID No. 1, SEQ ID No. 2, SEQ ID No. 3, and SEQ ID No. 7, respectively; or (ii) displays at least 80% homology with one or more of said amino acid sequences; and/or displays immunological cross-reactivity with an antibody raised against an α -amylase having one of said amino acid sequences; and/or is encoded by a DNA sequence which hybridizes with the same probe as a DNA sequence encoding an α -amylase having one of said amino acid sequences; in which variant:
 - (a) at least one amino acid residue of said parent α -amylase has been deleted; and/or
 - (b) at least one amino acid residue of said parent α -amylase has been replaced by a different amino acid residue; and/or
 - (c) at least one amino acid residue has been inserted relative to said parent α -amylase; said variant having α -amylase activity and exhibiting at least one of the following properties relative to said parent α -amylase: increased thermostability; increased stability towards oxidation; and reduced Ca^{2+} dependency; provided that the amino acid sequence of said variant is not identical to any of the amino acid sequences shown in SEQ ID No. 1, SEQ ID No. 2, SEQ ID No. 3 and SEQ ID No. 7, respectively.
2. A variant according to claim 1, wherein at least one oxidizable amino acid residue of said parent α -amylase has been deleted or has been replaced by a different amino acid residue which is less susceptible to oxidation than said oxidizable amino acid residue.
3. A variant according to claim 2, wherein said oxidizable amino acid residue is selected from the group consisting of methionine, tryptophan, cysteine and tyrosine.
4. A variant according to claim 2, wherein said oxidizable amino acid residue is a methionine which is, or which is equivalent to, M9, M10, M105, M202, M208, M261, M309, M382, M430 or M440 of the amino acid sequence shown in SEQ ID No. 1.
5. A variant according to claim 4, comprising a methionine substitution which is, or which is equivalent to, one of the following substitutions in the amino acid sequence shown in SEQ ID No. 1: M9L; M10L; M105L; M202L, T, F, I, V; M208L; M261L; M309L; M382L; M430L; M440L.

6. A variant according to claim 3, wherein a said methionine residue has been replaced by threonine.

7. A variant according to claim 1, wherein at least one amino acid which is, or which is equivalent to, F180, R181, G182, T183, G184 or K185 of the amino acid sequence shown in SEQ ID No. 1 has been deleted.

8. A variant according to claim 7, wherein the deleted amino acids are, or are equivalent to, any two of said amino acid residues.

9. A variant according to claim 8, wherein the deletions are, or are equivalent to, R181* + G182*; or T183* + G184*.

10. A variant according to claim 1, comprising an amino acid substitution which is, or which is equivalent to, one of the following substitutions in the amino acid sequence shown in SEQ ID No. 1: K269R; P260E; R124P; M105F,I,L,V; M208F,W,Y; L217I; V206I,L,F.

11. A variant according to claim 1, comprising an amino acid substitution which is, or which is equivalent to, one of the following substitutions in the amino acid sequence shown in SEQ ID No. 1: Y243F; K108R; K179R; K239R; K242R; K269R; D163N; D188N; D192N; D199N; D205N; D207N; D209N; E190Q; E194Q; N106D.

12. A DNA construct comprising a DNA sequence encoding an α -amylase variant according to claim 1.

13. A recombinant expression vector which carries a DNA construct according to claim 12.

14. A cell which is transformed with a DNA construct according to claim 12.

15. A cell according to claim 14, which is a microorganism.

16. A cell according to claim 15, which is a bacterium or a fungus.

17. A cell according to claim 16, which is a gram positive bacterium such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus laetus*, *Bacillus thuringiensis* or *Streptomyces lividans* or *Streptomyces murinus*, or a gram negative bacterium such as *E. coli*.

18. A method of producing an α -amylase variant, comprising culturing a cell according to claim 14 under conditions conducive to the production of the α -amylase variant, and recovering the α -amylase variant from the culture.

19. Use of an α -amylase variant according to claim 1 for washing and/or dishwashing.

20. A detergent additive comprising an α -amylase variant according to claim 1, optionally in the form of a non-dusting granulate, stabilized liquid or protected enzyme.

21. A detergent additive according to claim 20, comprising 0.02-200 mg of enzyme protein per gram of the additive.

22. A detergent additive according to claim 20, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

23. A detergent composition comprising an α -amylase variant according to claim 1 and a surfactant.

24. A detergent composition according to claim 23, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

25. A manual or automatic dishwashing detergent composition comprising an α -amylase variant according to claim 1 and a surfactant.

26. A dishwashing detergent composition according to claim 25, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.

27. A manual or automatic laundry washing composition comprising an α -amylase variant according to claim 1 and a surfactant.
28. A laundry washing composition according to claim 27, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, an amyloytic enzyme and/or a cellulase.
29. Use of an α -amylase variant according to claim 1 for textile desizing.

ADD
G